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## RAW SEQUENCE LISTING

DATE: 05/22/2003

PATENT APPLICATION: US/10/055,624B

TIME: 11:27:49

Input Set : A:\sequence listing 10-055,624 created 05-07-2003.txt  
 Output Set: N:\CRF4\05222003\J055624B.raw

3 <110> APPLICANT: Adams, Sean H  
 4 Chui, Clarissa  
 5 Goddard, Audrey D  
 6 Grimaldi, J. Christopher  
 8 <120> TITLE OF INVENTION: BFIT COMPOSITIONS AND METHODS OF USE  
 10 <130> FILE REFERENCE: 9800081-0066  
 12 <140> CURRENT APPLICATION NUMBER: 10/055,624B  
 13 <141> CURRENT FILING DATE: 2002-01-22  
 15 <150> PRIOR APPLICATION NUMBER: US 60/263,362  
 16 <151> PRIOR FILING DATE: 2002-01-22  
 18 <160> NUMBER OF SEQ ID NOS: 23  
 20 <170> SOFTWARE: PatentIn version 3.2  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1857  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <400> SEQUENCE: 1  
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 30 tctgtgttct ccaaccgcac atcccgaaag tcagccttac gtgcggggaa cgacagtgcc 120  
 32 atggcagacg gcgagggata cccgaacccc acggagggtgc agatgagccca gctgggtgctg 180  
 34 ccctgccaca ccaaccaacg tggtgagctg agcgtcgccc agctgctcaa gtggattgac 240  
 36 accacggctt gcctgtccgc ggagaggcac gctggctgcc cctgtgtcac agcttccatg 300  
 38 gatgacatct attttgagca caccattagt gttggacaag tggtaatata caaggccaag 360  
 40 gtgaaccggg cttcaactc cagcatggag gtggccatcc agtgtggccctc ggaggacctg 420  
 42 tgctctgaga agcagtggaa tgggtgcag gccttggcca cttcgtggc ccgcgcgagag 480  
 44 atcaccaagg tgaagctgaa gcagatcacg ccgcggacag aagaggagaa gatggagcac 540  
 46 agtgtggcgg ctgagcgcgc ggcgcacatgc cttgtctatg cagacaccat caaggacactc 600  
 48 ctggccaaact ggcgcattca gggcgatctg gagagcagag actgttagccg catgtgcgc 660  
 50 gctgagaaga cccgtgtgaa gagtgtggag ctggctctgc ctccccacgc caatcaccag 720  
 52 ggcaacaccc ttggggccca gatcatggcc tggatggaga atgtggccac cattgcagcc 780  
 54 agccggctct ggcgtgcccc ccctacgctg aaggccattt aatgttcca cttccgaggc 840  
 56 ccgtcccaagg tcggcgaccg tctggtgctc aaagccatcg tgaacaatgc cttcaaacat 900  
 58 agcatggagg tggcggtgtg cgtggaggcc tatcgccagg aggctgagac ccaccggcgc 960  
 60 cacatcaaca gtgcctttat gacctttgtg gtcctggacg cagatgacca gccccagttg 1020  
 62 ctgccctgga ttggccccc gcccggcgat ggtgacgcgc ggtaccgaga ggcgcgtgcc 1080  
 64 agaaaagaaga tccgcctgga caggaagtac atcggtgtct gtaagcagac agaggtgccc 1140  
 66 ctctccgtcc cctgggaccc tagcaaccag gtgtacctga gctacaataa cgtctccctcc 1200  
 68 ttgaagatgc ttgtggccaa ggacaactgg gtgctgtctt cggagatcag tcaggtccgc 1260  
 70 ctgtacactc tggaggatga caagttcctc tccttccaca tggagatggt ggtgcattgt 1320  
 72 gatgcagccc aggccttct gctgctctcg gacctgcgtc agaggccaga gtgggacaag 1380  
 74 cactaccgga ggcgtggagct agtgcagcac gtagacgagg acgacccat ctaccacgtc 1440  
 76 accagccctg ccctcggagg tcacacaaag ccccaggact tcgtgtatcc ggcctcgagg 1500  
 78 cggaaaggctt gtgacaatgg ggaccctat gtcatcgccg tggaggtcggt cacgctgccc 1560

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80 acacaccgag agacgccaga gtacagacgc ggagagaccc tctgctcagg ctttcgcctc 1620  
 82 tggcgcgagg gggaccagct gaccaagtgc tgctgggta gggctccct gactgagctg 1680  
 84 gtctcggcaa gtggcttcta ttcctgggg ctcgaatcca ggtcaaaaggg tcgcaggagc 1740  
 86 gacggttggaa atggaaaact agctggagga cacctgagta ctcttaaagc aatccccgtg 1800  
 88 gccaaaatca acagccgatt tggatacctt caagacacctt gaaaccttat catgagc 1857  
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 92 <211> LENGTH: 607  
 93 <212> TYPE: PRT  
 94 <213> ORGANISM: Homo sapiens  
 96 <400> SEQUENCE: 2  
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 99 1 5 10 15  
 102 Phe Ser Asn Arg Thr Ser Arg Lys Ser Ala Leu Arg Ala Gly Asn Asp  
 103 20 25 30  
 106 Ser Ala Met Ala Asp Gly Glu Gly Tyr Arg Asn Pro Thr Glu Val Gln  
 107 35 40 45  
 110 Met Ser Gln Leu Val Leu Pro Cys His Thr Asn Gln Arg Gly Glu Leu  
 111 50 55 60  
 114 Ser Val Gly Gln Leu Leu Lys Trp Ile Asp Thr Thr Ala Cys Leu Ser  
 115 65 70 75 80  
 118 Ala Glu Arg His Ala Gly Cys Pro Cys Val Thr Ala Ser Met Asp Asp  
 119 85 90 95  
 122 Ile Tyr Phe Glu His Thr Ile Ser Val Gly Gln Val Val Asn Ile Lys  
 123 100 105 110  
 126 Ala Lys Val Asn Arg Ala Phe Asn Ser Ser Met Glu Val Gly Ile Gln  
 127 115 120 125  
 130 Val Ala Ser Glu Asp Leu Cys Ser Glu Lys Gln Trp Asn Val Cys Lys  
 131 130 135 140  
 134 Ala Leu Ala Thr Phe Val Ala Arg Arg Glu Ile Thr Lys Val Lys Leu  
 135 145 150 155 160  
 138 Lys Gln Ile Thr Pro Arg Thr Glu Glu Lys Met Glu His Ser Val  
 139 165 170 175  
 142 Ala Ala Glu Arg Arg Arg Met Arg Leu Val Tyr Ala Asp Thr Ile Lys  
 143 180 185 190  
 146 Asp Leu Leu Ala Asn Cys Ala Ile Gln Gly Asp Leu Glu Ser Arg Asp  
 147 195 200 205  
 150 Cys Ser Arg Met Val Pro Ala Glu Lys Thr Arg Val Glu Ser Val Glu  
 151 210 215 220  
 154 Leu Val Leu Pro Pro His Ala Asn His Gln Gly Asn Thr Phe Gly Gly  
 155 225 230 235 240  
 158 Gln Ile Met Ala Trp Met Glu Asn Val Ala Thr Ile Ala Ala Ser Arg  
 159 245 250 255  
 162 Leu Cys Arg Ala His Pro Thr Leu Lys Ala Ile Glu Met Phe His Phe  
 163 260 265 270  
 166 Arg Gly Pro Ser Gln Val Gly Asp Arg Leu Val Leu Lys Ala Ile Val  
 167 275 280 285  
 170 Asn Asn Ala Phe Lys His Ser Met Glu Val Gly Val Cys Val Glu Ala  
 171 290 295 300  
 174 Tyr Arg Gln Glu Ala Glu Thr His Arg Arg His Ile Asn Ser Ala Phe

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Input Set : A:\sequence listing 10-055,624 created 05-07-2003.txt  
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175	305	310	315	320
178	Met Thr Phe Val Val Leu Asp Ala Asp Asp Gln Pro Gln Leu Leu Pro			
179		325	330	335
182	Trp Ile Arg Pro Gln Pro Gly Asp Gly Glu Arg Arg Tyr Arg Glu Ala			
183		340	345	350
186	Ser Ala Arg Lys Lys Ile Arg Leu Asp Arg Lys Tyr Ile Val Ser Cys			
187		355	360	365
190	Lys Gln Thr Glu Val Pro Leu Ser Val Pro Trp Asp Pro Ser Asn Gln			
191		370	375	380
194	Val Tyr Leu Ser Tyr Asn Asn Val Ser Ser Leu Lys Met Leu Val Ala			
195		385	390	395
198	Lys Asp Asn Trp Val Leu Ser Ser Glu Ile Ser Gln Val Arg Leu Tyr			
199		405	410	415
202	Thr Leu Glu Asp Asp Lys Phe Leu Ser Phe His Met Glu Met Val Val			
203		420	425	430
206	His Val Asp Ala Ala Gln Ala Phe Leu Leu Leu Ser Asp Leu Arg Gln			
207		435	440	445
210	Arg Pro Glu Trp Asp Lys His Tyr Arg Ser Val Glu Leu Val Gln Gln			
211		450	455	460
214	Val Asp Glu Asp Asp Ala Ile Tyr His Val Thr Ser Pro Ala Leu Gly			
215		465	470	475
218	Gly His Thr Lys Pro Gln Asp Phe Val Ile Leu Ala Ser Arg Arg Lys			
219		485	490	495
222	Pro Cys Asp Asn Gly Asp Pro Tyr Val Ile Ala Leu Arg Ser Val Thr			
223		500	505	510
226	Leu Pro Thr His Arg Glu Thr Pro Glu Tyr Arg Arg Gly Glu Thr Leu			
227		515	520	525
230	Cys Ser Gly Phe Cys Leu Trp Arg Glu Gly Asp Gln Leu Thr Lys Cys			
231		530	535	540
234	Cys Trp Val Arg Val Ser Leu Thr Glu Leu Val Ser Ala Ser Gly Phe			
235		545	550	555
238	Tyr Ser Trp Gly Leu Glu Ser Arg Ser Lys Gly Arg Arg Ser Asp Gly			
239		565	570	575
242	Trp Asn Gly Lys Leu Ala Gly Gly His Leu Ser Thr Leu Lys Ala Ile			
243		580	585	590
246	Pro Val Ala Lys Ile Asn Ser Arg Phe Gly Tyr Leu Gln Asp Thr			
247		595	600	605
250	<210> SEQ ID NO: 3			
251	<211> LENGTH: 1818			
252	<212> TYPE: DNA			
253	<213> ORGANISM: Homo sapiens			
255	<400> SEQUENCE: 3			
256	gtggattgc ccttgcattc aaatgatcca gaatgtcgga aatcacctgc gacggggctt			60
258	ggcctctgtt ttctccaacc gcacatcccg gaagtgcggcc ttacgtgcgg ggaacgcacag			120
260	tgcctatggca gacggcgagg gataccggaa ccccacggag gtgcagatga gccagctgg			180
262	gctgccctgc cacaccaacc aacgtggta gctgagcgtc gggcagctgc tcaagtggat			240
264	tgacaccacg gcttgcctgt ccgcggagag gcacgcgtgc tgccctgtg tcacagcttc			300
266	catggatgac atctatttg agcacaccat tagtgttgg acaagtggta atatcaaggc			360
268	caaggtgaac cgggcattca actccagcat ggaggtggc atccaggtgg cctcggagga			420

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270 cctgtgctct gagaagcagt ggaatgtgtg caaggccttg gccacccctcg tggcccgccg 480  
 272 agagatcacc aaggtaagc tgaagcagat cacggccgcg acagaagagg agaagatgga 540  
 274 gcacagtgtg gcggctgagc gccggcgcac ggccttgc tatgcagaca ccatcaagga 600  
 276 cctcctggcc aactgcgcca ttcaggggca tctggagagc agagactgtt gcccattgtt 660  
 278 gccggcttag aagaccctgt tggagaggtt ggagctgtt ctgcctcccc acgccaatca 720  
 280 ccagggcaac accttgggg gccagatcat ggcctggatg gagaatgtgg ccaccattgc 780  
 282 agccagccgg ctctgcccgtt cccaccctac gctgaaggcc attgaaatgtt tccacttccg 840  
 284 aggcccgtcc caggtcggcg accgtctgtt gctcaaagcc atcgtgaaca atgccttcaa 900  
 286 acatagcatg gaggtggcg tgcgttgg ggcctatcgc caggaggctg agacccaccg 960  
 288 gcccacatc aacagtgcct ttatgacctt tgcgttgc gacgcagatg accagcccc 1020  
 290 gttgctgccc tggattcggc cccagccccg cgatggttag cggcggtacc gagaggccag 1080  
 292 tgccagaaag aagatccgccc tggacagggaa gtacatcgtt tcctgttaagc agacagaggt 1140  
 294 gcccctctcc gtcccctggg acccttagcaa ccaggtgtac ctgagctaca ataacgtctc 1200  
 296 ctccctgaag atgctgtgg ccaaggacaa ctgggtgtt tcctcgagaa tcagtcagg 1260  
 298 cccctgtac actctggagg atgacaaggctt cctctccctt ccatggaga tgggtgtca 1320  
 300 tggatgca gcccaggcct tcctgtgtt ctcggacctg cgtcagaggc cagagtggg 1380  
 302 caagcactac cggagcgtgg agctagtgc gcaaggtagac gaggacgacg ccatctacca 1440  
 304 cgtcaccacg cctgcctcg gaggtcacac aaagccccag gacttcgtga tcctggcctc 1500  
 306 gaggcggaaag cttgtgaca atggggaccc ctatgtcatc ggcctgaggc cggtcacgct 1560  
 308 gcccacacac cgagagacgc cagagtacag acggcggagag accctctgtt caggcttctg 1620  
 310 cctctggcgc gagggggacc agctgaccaa ggtatcctac tacaaccagg ccaccccccagg 1680  
 312 tggatgcaac tatgtgacca ccaacgtgc cggcctctcc tctgagttt acaccac 1740  
 314 caaggctgtt gggatttc tcttgacaa ccggaaatgtt ctggcccccgc gcctccagac 1800  
 316 cctctagatg ccctcagc 1818

319 &lt;210&gt; SEQ ID NO: 4

320 &lt;211&gt; LENGTH: 594

321 &lt;212&gt; TYPE: PRT

322 &lt;213&gt; ORGANISM: Homo sapiens

324 &lt;400&gt; SEQUENCE: 4

326 Met Ile Gln Asn Val Gly Asn His Leu Arg Arg Gly Leu Ala Ser Val  
 327 1 5 10 15  
 330 Phe Ser Asn Arg Thr Ser Arg Lys Ser Ala Leu Arg Ala Gly Asn Asp  
 331 20 25 30  
 334 Ser Ala Met Ala Asp Gly Glu Gly Tyr Arg Asn Pro Thr Glu Val Gln  
 335 35 40 45  
 338 Met Ser Gln Leu Val Leu Pro Cys His Thr Asn Gln Arg Gly Glu Leu  
 339 50 55 60  
 342 Ser Val Gly Gln Leu Leu Lys Trp Ile Asp Thr Thr Ala Cys Leu Ser  
 343 65 70 75 80  
 346 Ala Glu Arg His Ala Gly Cys Pro Cys Val Thr Ala Ser Met Asp Asp  
 347 85 90 95  
 350 Ile Tyr Phe Glu His Thr Ile Ser Val Gly Gln Val Val Asn Ile Lys  
 351 100 105 110  
 354 Ala Lys Val Asn Arg Ala Phe Asn Ser Ser Met Glu Val Gly Ile Gln  
 355 115 120 125  
 358 Val Ala Ser Glu Asp Leu Cys Ser Glu Lys Gln Trp Asn Val Cys Lys  
 359 130 135 140  
 362 Ala Leu Ala Thr Phe Val Ala Arg Arg Glu Ile Thr Lys Val Lys Leu  
 363 145 150 155 160

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366 Lys Gln Ile Thr Pro Arg Thr Glu Glu Glu Lys Met Glu His Ser Val  
 367 165 170 175  
 370 Ala Ala Glu Arg Arg Arg Met Arg Leu Val Tyr Ala Asp Thr Ile Lys  
 371 180 185 190  
 374 Asp Leu Leu Ala Asn Cys Ala Ile Gln Gly Asp Leu Glu Ser Arg Asp  
 375 195 200 205  
 378 Cys Ser Arg Met Val Pro Ala Glu Lys Thr Arg Val Glu Ser Val Glu  
 379 210 215 220  
 382 Leu Val Leu Pro Pro His Ala Asn His Gln Gly Asn Thr Phe Gly Gly  
 383 225 230 235 240  
 386 Gln Ile Met Ala Trp Met Glu Asn Val Ala Thr Ile Ala Ala Ser Arg  
 387 245 250 255  
 390 Leu Cys Arg Ala His Pro Thr Leu Lys Ala Ile Glu Met Phe His Phe  
 391 260 265 270  
 394 Arg Gly Pro Ser Gln Val Gly Asp Arg Leu Val Leu Lys Ala Ile Val  
 395 275 280 285  
 398 Asn Asn Ala Phe Lys His Ser Met Glu Val Gly Val Cys Val Glu Ala  
 399 290 295 300  
 402 Tyr Arg Gln Glu Ala Glu Thr His Arg Arg His Ile Asn Ser Ala Phe  
 403 305 310 315 320  
 406 Met Thr Phe Val Val Leu Asp Ala Asp Asp Gln Pro Gln Leu Leu Pro  
 407 325 330 335  
 410 Trp Ile Arg Pro Gln Pro Gly Asp Gly Glu Arg Arg Tyr Arg Glu Ala  
 411 340 345 350  
 414 Ser Ala Arg Lys Lys Ile Arg Leu Asp Arg Lys Tyr Ile Val Ser Cys  
 415 355 360 365  
 418 Lys Gln Thr Glu Val Pro Leu Ser Val Pro Trp Asp Pro Ser Asn Gln  
 419 370 375 380  
 422 Val Tyr Leu Ser Tyr Asn Asn Val Ser Ser Leu Lys Met Leu Val Ala  
 423 385 390 395 400  
 426 Lys Asp Asn Trp Val Leu Ser Ser Glu Ile Ser Gln Val Arg Leu Tyr  
 427 405 410 415  
 430 Thr Leu Glu Asp Asp Lys Phe Leu Ser Phe His Met Glu Met Val Val  
 431 420 425 430  
 434 His Val Asp Ala Ala Gln Ala Phe Leu Leu Leu Ser Asp Leu Arg Gln  
 435 435 440 445  
 438 Arg Pro Glu Trp Asp Lys His Tyr Arg Ser Val Glu Leu Val Gln Gln  
 439 450 455 460  
 442 Val Asp Glu Asp Asp Ala Ile Tyr His Val Thr Ser Pro Ala Leu Gly  
 443 465 470 475 480  
 446 Gly His Thr Lys Pro Gln Asp Phe Val Ile Leu Ala Ser Arg Arg Lys  
 447 485 490 495  
 450 Pro Cys Asp Asn Gly Asp Pro Tyr Val Ile Ala Leu Arg Ser Val Thr  
 451 500 505 510  
 454 Leu Pro Thr His Arg Glu Thr Pro Glu Tyr Arg Arg Gly Glu Thr Leu  
 455 515 520 525  
 458 Cys Ser Gly Phe Cys Leu Trp Arg Glu Gly Asp Gln Leu Thr Lys Val  
 459 530 535 540  
 462 Ser Tyr Tyr Asn Gln Ala Thr Pro Gly Val Leu Asn Tyr Val Thr Thr

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/055,624B

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Input Set : A:\sequence listing 10-055,624 created 05-07-2003.txt  
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